REMARKS

The Examiner alleges that original claims 1-41 are drawn to five patentably distinct inventions.

I. Claims 1-11, 15-34, drawn to a nucleic acid encoding an ISUM2A polypeptide, a vector, host cell, plant, and seed comprising said nucleic acid, and a method of making a transformed plant comprising said nucleic acid, has been classified in class 800, subclass 290.

II. Claims 12-14, drawn to primers and a method using the primers to detect the presence of an ISUM2A polypeptide in a sample, is classified in class 536, subclass 24.33.

III. Claims 35-36, drawn to an ISUM2A polypeptide, has been classified in class 530, subclass 350.

IV. Claims 37-39, drawn to an antibody directed against an ISUM2A polypeptide and a method and kit for detecting said polypeptide, has been classified in class 530, subclass 387.1.

V. Claims 40-41, drawn to the use of a nucleic acid in selection programs and a method for selecting plants with modified embryo size, has been classified in class 435, subclass 6.

The Examiner alleges that Group I Claims 1-11, 15-34, drawn to a nucleic acid encoding an ISUM2A polypeptide, a vector, host cell, plant, and seed comprising said nucleic acid, and a method of making a transformed plant comprising said nucleic acid, classified in class 800, subclass 290, is patentably distinct from Group II Claims 12-14, drawn to primers and a method using the primers to detect the presence of an ISUM2A polypeptide in a sample, classified in class 536, subclass 24.33.

It is alleged that Group I and Group II inventions are distinct from each other because:

- A search for the method of group I will require a sequence search for nucleic acids encoding ISUM2A and a search of methods for plant transformation and heterologous expression of proteins in plants whereas a search for the methods of group II will require searching for methods of detecting proteins using primers.
- Further that the method of group I is patentably distinct from the methods of groups II because it requires different starting materials and involves different methods steps. The methods of groups II require primers rather than a polynucleotide encoding a full-length protein. The method of group I involves method steps for generating a transgenic plant, whereas the methods of groups II involve methods for detection.
- A search for the method of group I will require a sequence search for nucleic acids encoding ISUMZA and a search of methods for plant transformation and heterologous expression of proteins in plants. A search for the method of groups II will require a sequence search of the nucleic acid databases specifically for primers which will involve a score over length analysis. A search for the methods of group II will require searching for methods of detecting proteins using primers.

Examiner has also applied an additional restriction of the claims alleging that the Application contains claims directed to multiple polynucleotide molecules. It is further alleged that each of these polynucleotides are patentably distinct from each other because the polynucleotides are each unique molecules with different chemical and structural features and so are deemed to normally constitute independent and distinct inventions subject to a restriction

requirement pursuant to 35 U.S.C. § 121 and 37 C.F.R. § 1.141 *et seq*. The Examiner has required Applicants to select one group of nucleic acid and amino acid sequences from the following:

A) SEQ ID NOS: 1, 3, and 5

B) SEQ ID NOS: 2, 4, and 6.

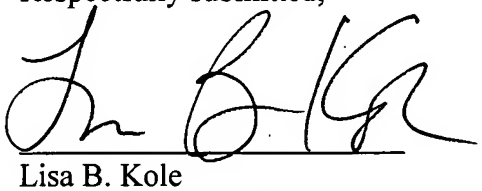
In response to the general restriction requirement, Applicants respectfully disagree and suggest that Group I and Group II claims of the present Application are directed to a single invention. Claims 1-11 and 15-34 are directed toward production of transgenic plant or plant cell encoding an ISUM2A polypeptide with specific desired characteristics. Group II Claims 12-14 are directed to a method for identifying or screening for the transgene positive plant of Group I claims using a polynucleotide sequence. Both Group I and II claims will require a search of nucleic acid sequences. In addition, both Group I and II use polynucleotide sequences encoding an ISUM2A polypeptide and since Group I requires a sequence search for nucleic acids encoding ISUM2A, Group II polypeptides while smaller in size than Group I is likely to be part of the same search strategy due to high sequence homology. The Examiner states that Group II claims require a search of the nucleic acid databases specifically for primers which will involve a score over length analysis and for methods of detecting proteins using primers. Group II claims are directed to methods of detecting ISUM2A nucleic acid molecules of Group I Claims under conditions permitting specific hybridization. Thus in addition to the fact that a search of sequences in Group I claims will likely encompass sequences in Group II claims, only routine methods of hybridization are additionally specified in Group II claims. Thus, contrary to the Examiner's basis for restriction, Applicants suggest that examining both

Groups would not constitute an undue burden to examine more than one invention.

In order to be fully responsive to the requirement for restriction, Applicants elect to pursue the claims of Group I (1-11, 15-34) with traverse and without prejudice to purse the withdrawn claims in one or more divisional applications. Applicants select SEQ ID NO:5 and SEQ ID NO:6 without traverse and without prejudice to purse the withdrawn sequences in one or more divisional applications. Applicants respectfully request that the Examiner also examine Group II Claims 12-14, in addition to Group I Claims 1-11, 15-34.

If any additional fee is due, or if any overpayment has been made, in connection with the filing of this response, the Commissioner is authorized to charge any such fee or credit any overpayment, to our Deposit Account No. 02-4377. A duplicate copy of this paper is enclosed.

Respectfully submitted,

By: 

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